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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 04:28:16 ; Search time 49 Seconds

(without alignments)
372.766 Million cell updates/sec

Title: US-09-895-298A-83

Perfect score: 1002

Sequence: 1 MMNFQPPSKAWRASQMTFF.....HDGSLDLRSKRSVQEGNPRA 190

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	99.5	9.9	1203	2	H89606	protein B0416.1 (1
2	94.5	9.4	451	2	A96920	probable ABC trans
3	88	8.8	322	2	C70905	hypothetical prote
4	87.5	8.7	261	2	T20264	hypothetical prote
5	87	8.7	272	2	H85355	senescence-associ
6	84.5	8.4	713	2	H83684	hypothetical prote
7	84	8.4	399	2	D70072	antibiotic resista
8	81.5	8.1	154	2	AD1677	signal peptidase I
9	81.5	8.1	261	2	AH2288	hypothetical prote
10	80.5	8.0	200	2	G83834	hypothetical prote
11	80	8.0	378	2	S61981	hypothetical prote
12	80	8.0	443	2	B26696	probable membrane
13	79.5	7.9	154	2	AD1305	hypothetical prote
14	79.5	7.9	217	2	AC2538	signal peptidase I
15	79.5	7.9	396	2	H89869	hypothetical prote
16	79.5	7.9	772	2	E96977	hypothetical prote
17	79	7.9	239	2	AD0593	hypothetical prote
18	78.5	7.8	229	2	G90027	pnuic protein [limp
19	78	7.8	319	2	T21402	urease accessory p
20	77.5	7.7	306	2	D71609	hypothetical prote
21	77.5	7.7	515	2	AF2321	hypothetical prote
22	77.5	7.7	604	2	G89864	hypothetical prote
23	77	7.7	288	2	S36956	cytochrome-c oxida
24	77	7.7	342	2	A38908	spa40 protein - Sh
25	77	7.7	392	2	F84566	hypothetical prote
26	77	7.7	564	2	F90965	hypothetical prote
27	77	7.7	564	2	F85813	hypothetical prote
28	77	7.7	605	2	H71562	probable flagellar
29	76.5	7.6	176	2	AD0072	probable membrane

30	76.5	7.6	322	2	D37753	PnuC protein - Sal
31	76	7.6	447	2	D81336	probable K+ uptake
32	76	7.6	569	2	H64959	probable membrane
33	76	7.6	661	2	T47467	hypothetical prote
34	75.5	7.5	703	2	T24975	hypothetical prote
35	75.5	7.5	975	2	T16073	hypothetical prote
36	75.5	7.5	1695	2	JE0084	voltage-gated sodi
37	75.5	7.5	2410	2	T43731	cell wall alpha-gl
38	75	7.5	175	2	H71896	hypothetical prote
39	75	7.5	175	2	F86764	hypothetical prote
40	75	7.5	445	2	E22845	hypothetical prote
41	75	7.5	1053	2	S58883	calcium-channel ho
42	74.5	7.4	148	1	T12787	hypothetical prote
43	74.5	7.4	267	2	A82997	hypothetical prote
44	74.5	7.4	308	2	H86268	hypothetical prote
45	74.5	7.4	348	2	AE0049	M48 peptidase fam1

ALIGNMENTS

RESULT 1

H89606

protein B0416.1 [imported] - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001

C/Accession: H89606

R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating bio

A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C-

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;

A/Accession: H89606

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1203 <STO>

A/Cross-references: GB:chr_X; PIDN:AB36841.2; PID:g4850180; GSPDB:GN00028; CESP:B041

A/Genetics:

A:Gene: B0416.1

A:Map position: X

Query Match

Best Local Similarity 9.9%; Score 99.5; DB 2; Length 1203;

Matches 39; Conservative 23; Mismatches 50; Indels 29; Gaps 8;

QY 6 PPSKAWRASQMTFFIFLFFPSFTGVLCTAI--TWRLKPSADCGPFGGLPLFIHSIV 63

Db 701 PASQIFRASRSNFFALLILFLF---LCTLPVGFVIASKTPSKCGPF-GNOSFFYSVI 756

QY 64 SWIDTLSTPPGYLWVWYRNLIQSVHFF-----ILTLYLITTYLKWQT---EG 112

Db 757 T--DVLEN-----LDKTLVNGIKYLSLPGIIPVLVLSLVYFLIAMVGLSQAN 806

QY 113 RKIMIRLHEQINEGKDKMF 133

Db 807 QDLISFOLMYER--TEKKKIF 825

RESULT 2

A96920

probable ABC transporter, permease component CAC0165 [imported] - Clostridium acetobu

C/Species: Clostridium acetobutylicum

C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C/Accession: A96920

R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L

.J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: A96920

A/Status: preliminary

A/Molecule type: DNA


```
Db      131 VIEKTIKIVASEVVKLYITTTKEGRFVEQDLHQQEGVDLPDIAIFGKEYKRPKYEIIRLIQ 190
        :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Yq      141 LQD-----MEKKANDSSLVERREVEOQGFLHGCHGSGLDRSRVSQESNPR 189
        :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      191 AADHEPVSLWFVEDRIKLTLQLVOQSDLED--VKLFADMGWYNTOSEKKAQSDPR 244

RESULT 10
G83834
hypothetical protein BH1479 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: G63834
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiroe, T.
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83834
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-200 <STO>
A:Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05198.1; GSFPDB:GN000004
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1479

Query Match          8.0%; Score 80.5; DB 2; Length 200;
Best Local Similarity 23.8%; Pred. No. 3.5;
Matches 36; Conservative 25; Mismatches 55; Indels 35; Gaps 6;

Yq      19 FFILLFFPSPFTG-----VLCTLA-----ITIMRLKPASDCGFPGPLPTFI 59
        ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      10 FFAMLLMTSFSQPILDFWIVFPISLVISAIAIFRSRIPPIKRKPPLTICGFALLSGLEL 69
        :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Yq      60 HSIVS---WDPLSTRDPGYLMVVYIRNLIGSVHFEEFILTLVLII--TYLW----- 107
        :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      70 YGLFAFGKWLTITLGPIPLLASLETLY-DMIRPTFMWHYEVLFVFILGEELFWRGYVGVT 128
        :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Yq      108 ---QTTEGRKIMIRLLHQIINECKDKMFLLI 135
        :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      129 LHQMSEGRAITFGALIXGVHAASSSLLEV 159

RESULT 11
S61981
probable membrane protein YOL003c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O2389; hypothetical protein UNE378
C:Species: Saccharomyces cerevisiae
C>Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 19-Apr-2002
A:Accession: S61981; S66684; S66685; S72130
R:Sterky, F.; Uhlen, M.
submitted to the EMBL Data Library, December 1995
A:Reference number: S61981
A:Accession: S61981
A:Molecule type: DNA
A:Residues: 1-378 <STE>
A:Cross-references: EMBL:U43491; NID:g1150992; PID:g1150993
R:Petersson, B.; Sterky, F.; Uhlen, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66682
A:Accession: S66684
A:Molecule type: DNA
A:Residues: 1-378 <PET>
A:Cross-references: EMBL:Z74745; NID:g1419764; PID:e251831; PID:g1419765; MIPS:YOL003c
A:Experimental source: strain S288C
R:Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66685
A:Accession: S66685
A:Molecule type: DNA
A:Residues: 1-378 <HUG>
A:Cross-references: EMBL:Z74745; NID:g1419764; PID:e251831; PID:g1419765; MIPS:YOL003c
```

A;Experimental source: strain S288C
R;Sterky, F.; Holmberg, A.; Petersson, B.; Uhlen, M.
Yeast 12, 1091-1095, 1996
A;Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Sacch
A;Reference number: S72130; MUID:97051599; PMID:8896276
A;Accession: S72130
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-378 <STM>
A;Cross-references: EMBL:U43491; NID:g1150992; PIDN:AAC49477.1; PID:g1150993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C;Genetics:
A;Cross-references: SGD:S0005363
A;Map position: 15L
A;Note: YOL003c

C;Keywords: transmembrane protein
F;10-26/Domain: transmembrane #status predicted <TM1>
F;124-140/Domain: transmembrane #status predicted <TM2>
F;173-189/Domain: transmembrane #status predicted <TM3>

Query Match 8.0%; Score 80; DB 2; Length 378;
Best Local Similarity 23.7%; Pred. No. 8.1;
Matches 41; Conservative 24; Mismatches 54; Indels 54; Gaps 9;

OY 3 NEQPPSKAWRASOMTFEFLFFPSF-----TGVLCITAI---TIWRLKPSADCG 50
|::|| | | | | | | | | | | | | | | | | |
Db NYKPPPDIMRN-----FCRKQOSYKPERSHHCKTCNQCLMDHHCPWTM----NCV 115

OY 51 PERGLPLFIHSIYSWIDLST----RPGYLWVWIYRNLIg-----SVHF 91
Db 116 GFANYPHFLRFMIIVTSVLFCIOAKRIYFIWOORHLPGVFKKSELIFLTISPLNS 175

OY 92 FEILTLIVLITYLYWOITEGRK----IMIRLHEQIIIEGDKMEFLIEKL 139
|::|| | | | | | | | | | | | | | | | | |
Db 176 FVLTTITLIFLNCLEFNQILNGRSQIESWDMDL--ESLFNSGR---LTQKLI 222

RESULT 12
B26696
hypothetical protein 1 (Cyb-COI intergenic region) - Leishmania tarentolae mitochond
C;Species: mitochondrion Leishmania tarentolae
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 07-Dec-1999
C;Accession: B26696
R;Simpson, L.; Neckelmann, N.; de la Cruz, V.F.; Simpson, A.M.; Feagin, J.E.; Jasmer,
J. Biol. Chem. 262, 6182-6196, 1987
A;Title: Comparison of the maxicircle (mitochondrial) genomes of Leishmania tarentola
A;Reference number: A92643; MUID:87194837; PMID:3032958
A;Accession: B26696
A;Molecule type: DNA
A;Residues: 1-443 <SIM>
A;Cross-references: GB:M10126; GB:J02707; GB:M10127; GB:M1022; GB:M64690; GB:N00030;
A;Note: the authors translated the codon ATT for residue 388 as Phe and TTC for resid
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: hypothetical protein 1 (Cyb-COI intergenic region)
C;Keywords: mitochondrion

Query Match 8.0%; Score 80; DB 2; Length 443;
Best Local Similarity 26.4%; Pred. No. 9.6;
Matches 28; Conservative 21; Mismatches 35; Indels 22; Gaps 4;

OY 20 FIFLFPSPFGVLCITAITIWRLKPSADCGPFRGLPLFIHSIYSWIDLSTRPGYLWV 79
|::|| | | | | | | | | | | | | | | | | |
Db 161 FCFLIFDEWGLICLCEFYILLIEK-----LYIALILFLFEQLYINLGVF--I 206

OY 80 WIYRNIGSVHFEILTLIVLITYLYWOITEGRKIMIRLHEQII 125
|::|| | | | | | | | | | | | | | | | | |
Db 207 FIY---MLTFVVLFCFILITILICFIYFI-----IFIKLIIIOSI 244

RESULT 13
ADI305

signal peptidase II homolog lsp [imported] - *Listeria monocytogenes* (strain EGD-e)
 C:Species: *Listeria monocytogenes*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C:Accession: AD1305
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entlian, K.D.; Eschl, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AD1305
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-154 <GLA>
 A:Cross-references: GB:NC_003210; PIDN:CAC99922.1; PID:gl6411298; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lsp
 C:Superfamily: lipoprotein signal peptidase

Query Match	7.9%	Score 79.5;	DB 2;	Length 154;
Best Local Similarity	21.6%;	Pred. No. 3.3;		
Matches 27;	Conservative 27;	Mismatches 22;	Indels 49;	Gaps 7;
QY 33	LCITAI-----TWRKPSADCGPFRGLPLFIHSIYSWIDTLSTPGYLWVWI-YRN-84			
	: : : :		: :	
Db 5	LITLAVIALDQLTKNIIVVQNMETG-----QKIEVIIPGLY--WISTYRND-46			
QY 85	-----LIGSVHFFFIITLAVL-IITFLYMQTFEGRKI-----MIRLLH-121			
	: : : : : : :			
Db 47	GAANSILEGHMMFFYLITVVVIGIITIMQKYAKGRKLFSSISLAFILGGAIGNFIDRVLH-106			
QY 122	EQIIN-126			
	: : : : :			
Db 107	QEVVD-111			

RESULT 14
AC2538
hypothetical protein all7590 [imported] - Nostoc sp. (strain PCC 7120) plasmid pcc7120be
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AC2538
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2538
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <KUR>
A:Cross-references: GB:AP003602; PIDN:BAB7233.1; PID:q17134675; GSPDB:GN00181
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all7590
A:Genome: plasmid

```

Query Matchin          7.9%; Score 79.5; DB 2; Length 217;
Best Local Similarity 23.8%; Pred. No. 4.8;
Matches 29; Conservative 17; Mismatches 35; Indels 41; Gaps 6;

QY 3 NQDPPS--KAMRASQMMTFETFLFPSPFTGVCLTALITIRLKPSADCCGPRGLPLFIH 60
   : : | : | | : | | | : | | | : | | | : | | | :
Db 26 SFTKPKSPRDMRAFGAFAFSAFIMALFTEMY-----GIPLTIT 61
   : : | : | | : | | | : | | | : | | | :

QY 61 SIYSW-----IDTLSTRGYLMVVMYIRNLIGSVHF--FFITLIVL---ITVLYW 107
   : : | : | | : | | | : | | | : | | | : | | | :
Db 62 LLSGWLQSRYPKLDLISHDVGLIM--WTMLGMGNPHFENVLIHINLLIGGFITLASAW 119

```

QY	108	QI	109
		:::	
Db	120	EV	121

RESULT 15

hypothetical protein SA0874 [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89869
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, M. A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
L:ncnt 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89869
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-396 <KUR>
A:Cross-references: GB:BA000018; PID:q13700819; PIDN:BAR42115.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0874

	Query Match	7.9%	Score 79.5;	DB 2;	Length 396;
	Best Local Similarity	23.0%;	Pred. No. 9.4;		
	Matches 35; Conservative	25;	Mismatches 39;	Indels 53;	Gaps
QY	22 FLLEFPSEFTGVLCTLAITWRLKPSADCGPFRGLPLFIHSIYS-----WIDTFLS 70				
	:	:		:	:
Db	86 FILAFIS-----LFLVIM-----FPSAPFYI--IFSAMMLGIASPIWIMLS 126				
QY	71 T-----RPGYLWVV-----IYRNLIQSVAH---FEFIIITLIVLIITYEYW---- 107				
	: :	:	:		
Db	127 SVEEDKRKGOMGIYFFSWLLGLLVGVAFMNLILIKVHPTRFAFMMSLVLIAMIYYFVDV 186				
QY	108 QITEGRKIMIRLLHEQIINEGKDKMFLIEKLI 139				
	:::	:		:::	
Db	187 KLTNYNTPRPVKAAQLRQIVDVTNRHLLEPGIL 218				

Search completed: November 9, 2002, 04:34:14
Job time : 52 secs

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